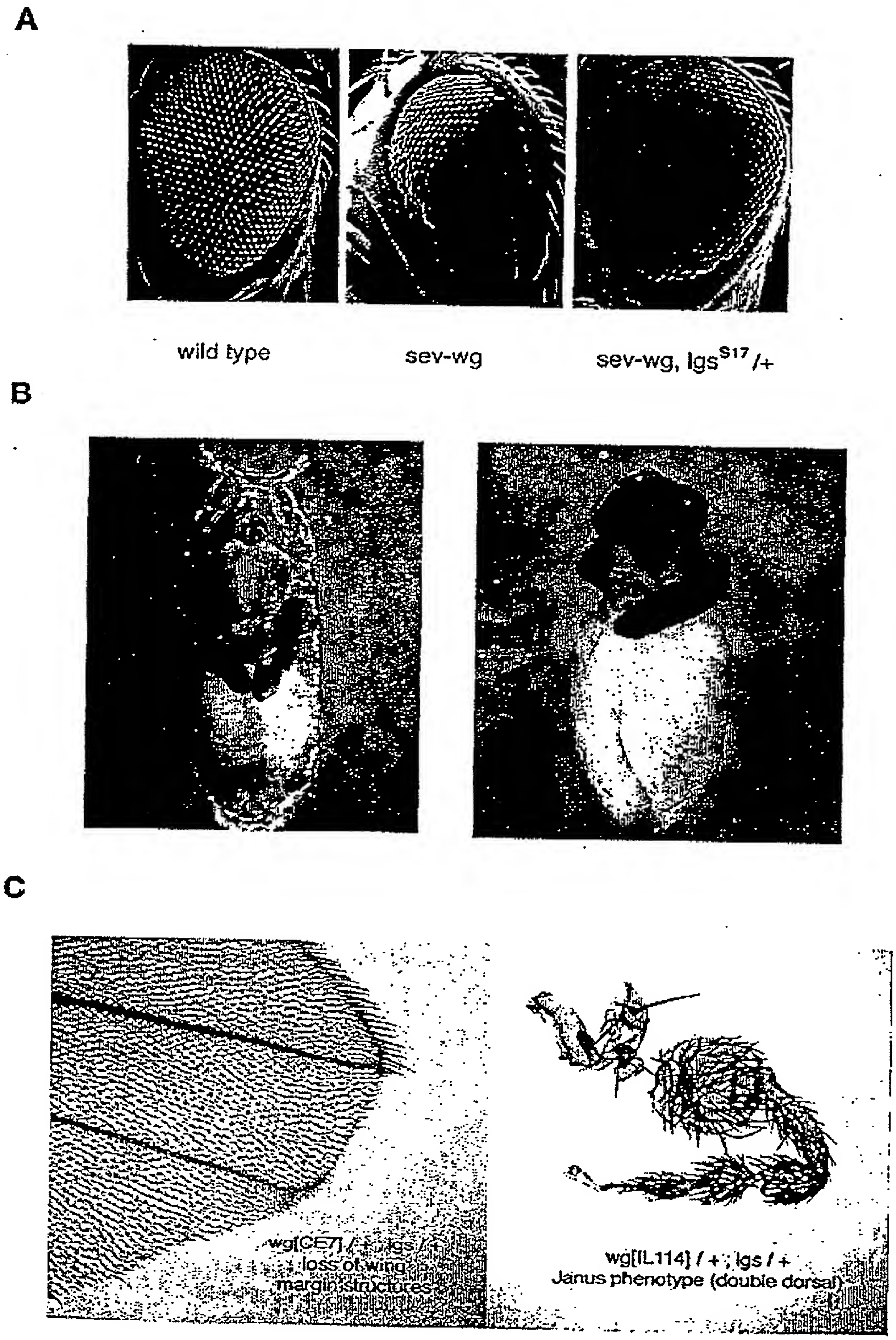
Figure 1


A
wild type
sev-wg
sev-wg, lgs^{S17}/+
B
C
wg[CE7] / + ; lgs / +
loss of wing
margin structures
wg[IL114] / + ; lgs / +
Janus phenotype (double dorsal)

09915543.072701

Figure 2

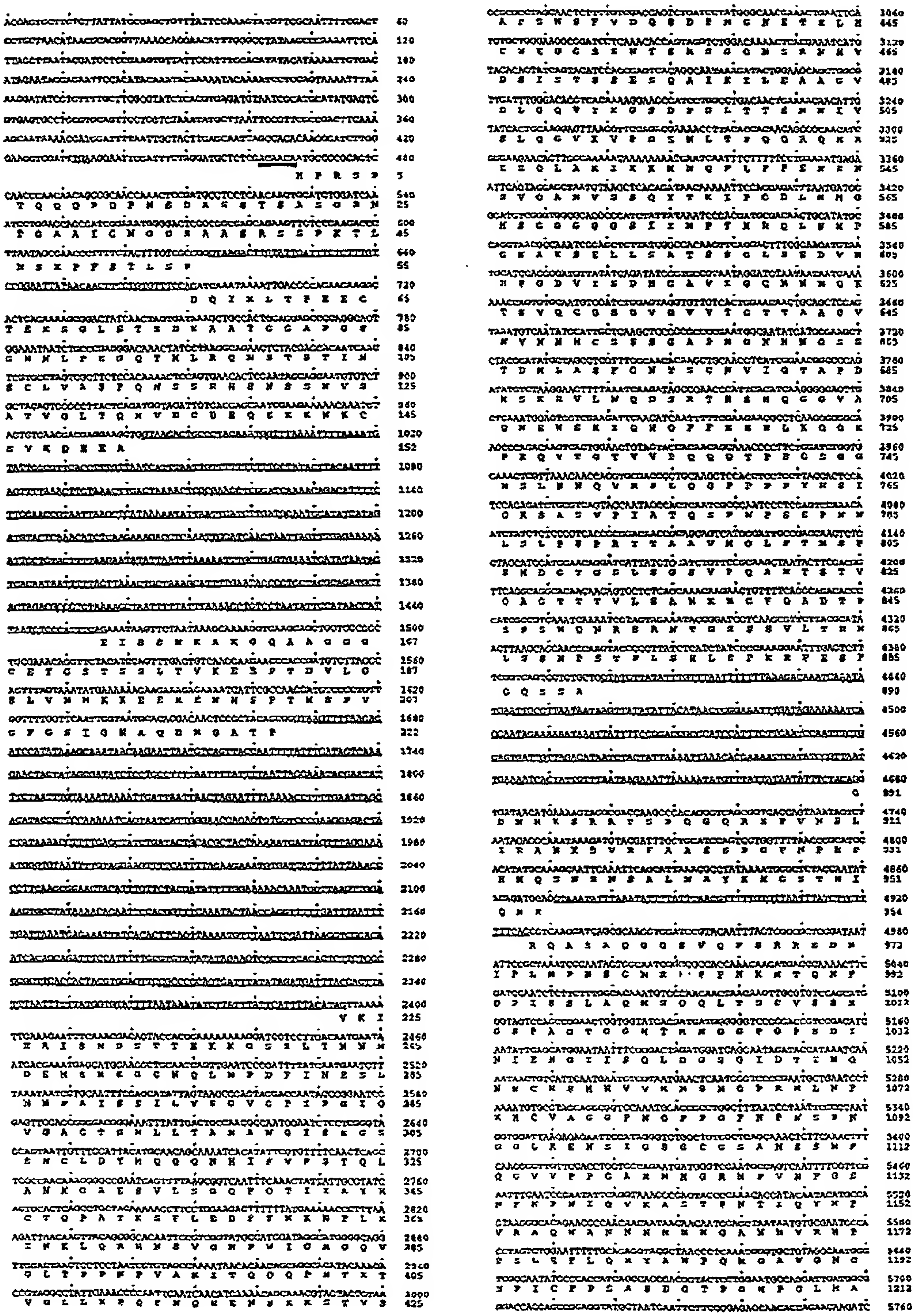
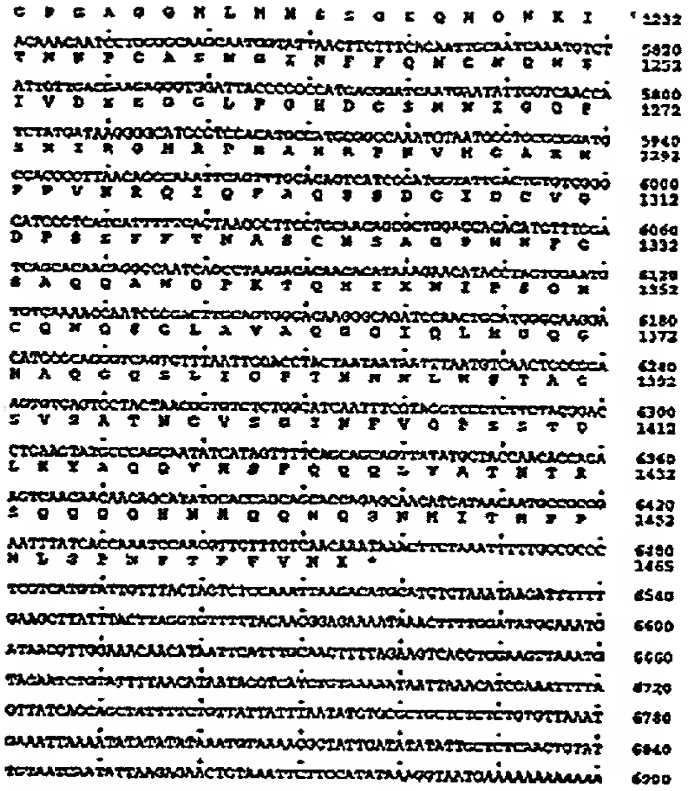


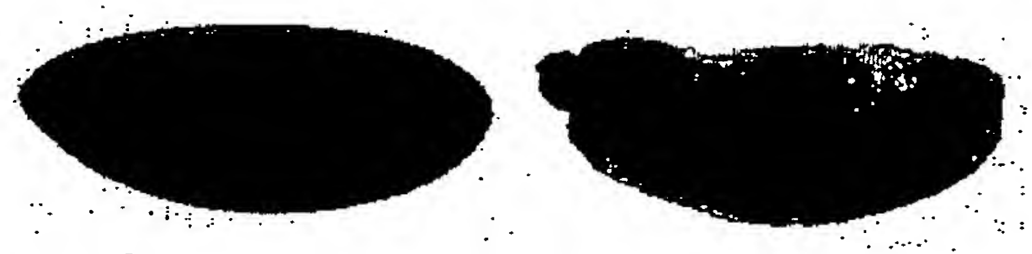
Figure 2: *legless*



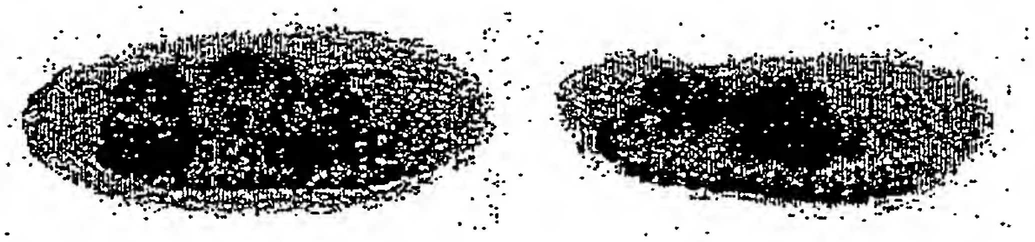
AAAAAAAA 6909

Figure 3

A



yw x lgs anti-sense



yw x lgs sense

B

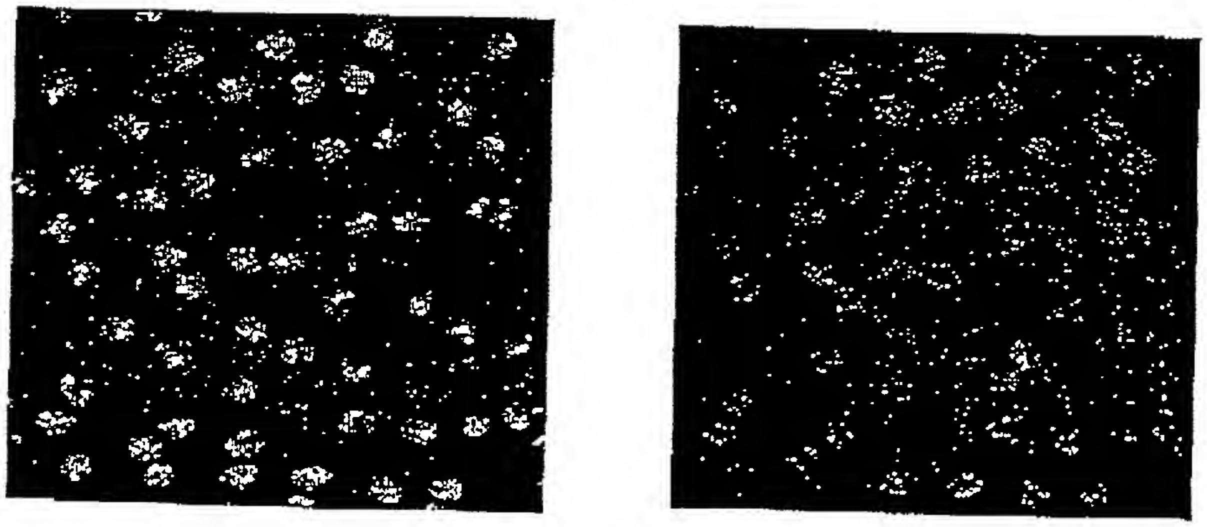


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Figure 4

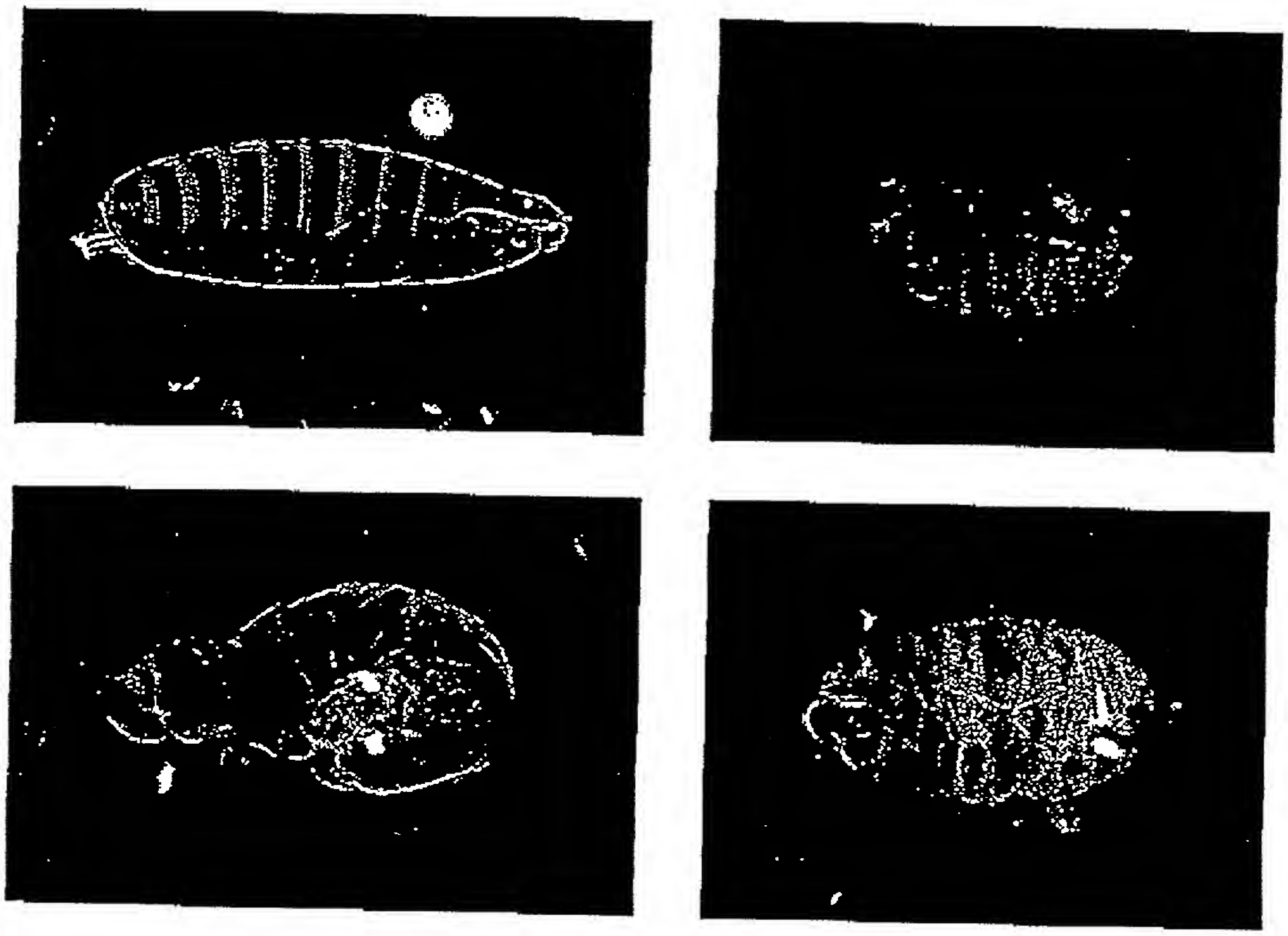

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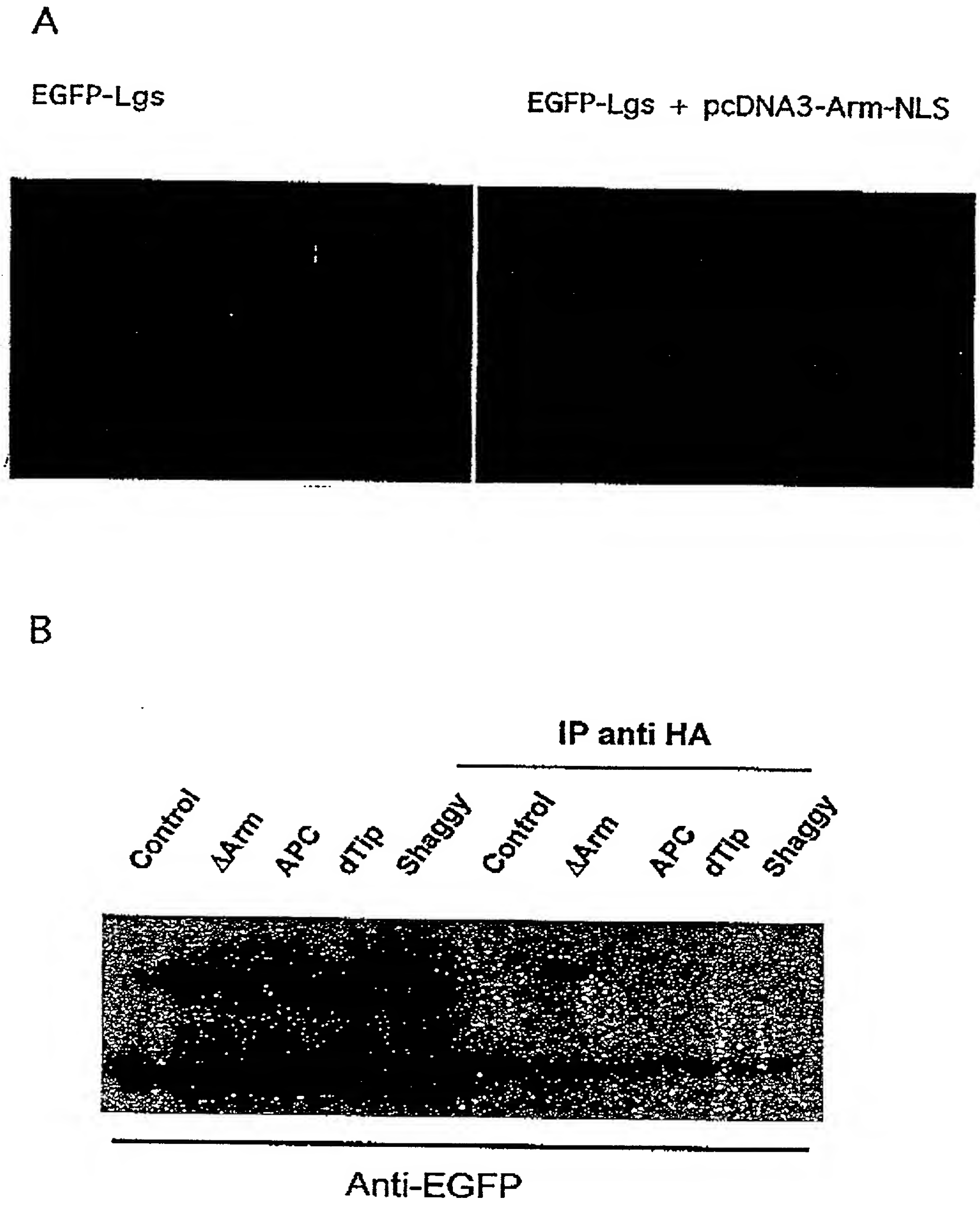
Figure 5


A
EGFP-Lgs
EGFP-Lgs + pcDNA3-Arm-NLS
B
IP anti HA
Control
ΔArm
APC
dTip
Shaggy
Control
ΔArm
APC
dTip
Shaggy
Anti-EGFP

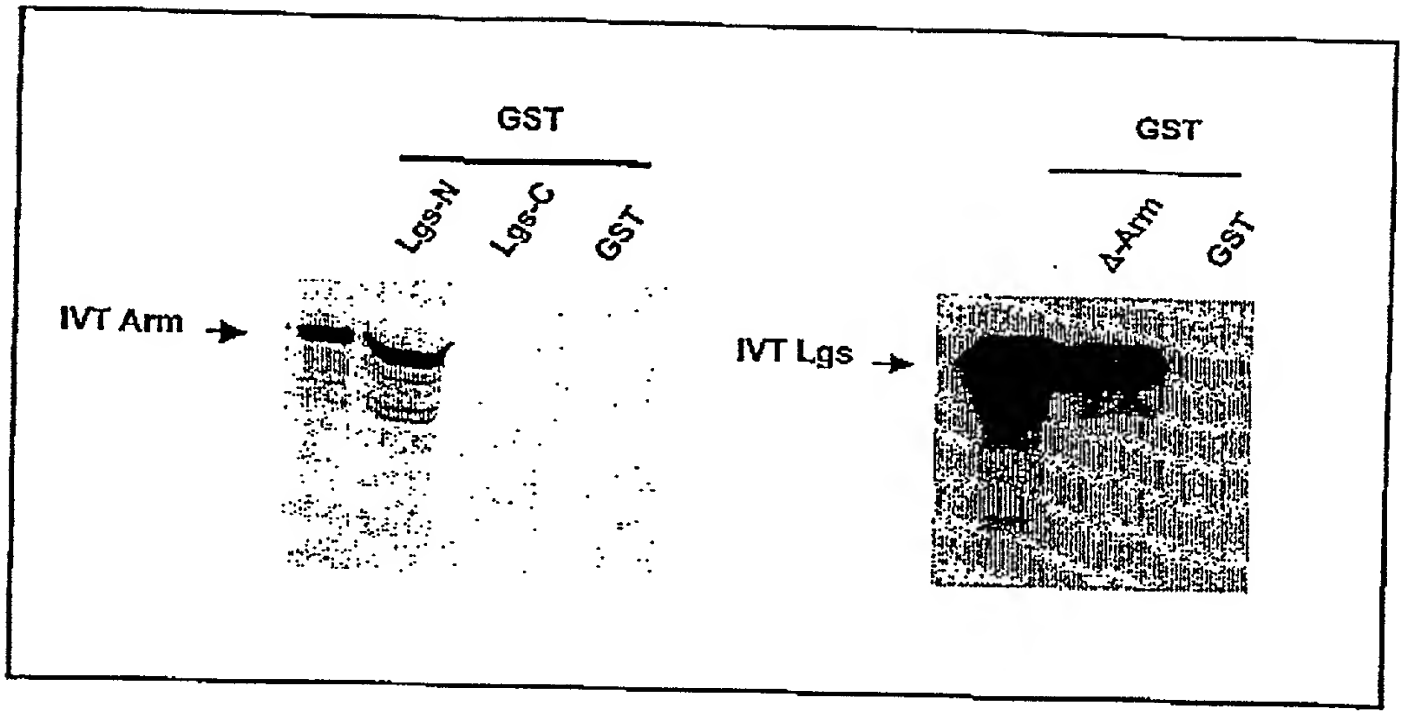
5C

		BAIT fusions: pLex						
		Lgs 1-1464	BCL9 199-392	BCL9 1-1426	Dco+	ΔArmC	Δß-Cat	Pan
PREY fusions: pJG4-5	lgs364-555					[illegible]		
	lgs1-385					[illegible]		
	lgs1-732					+		
	lgs364-1090					+		
	lgs726-1464					[illegible]		
	lgs1-1464				[illegible]	+	n.d.	-
	BCL9 199-392					+	n.d.	
	BCL91-1426					+	+	
	Dco+	-						
	DAxin	(+)				+		
	ΔArmC	+	+	+				[illegible]
	ß-Cat	+	+	+				
	Pan	+				+		
	pJG4-5	-	[illegible]	[illegible]		-	-	

+: interaction seen in yeast two-hybrid assay
-: no interaction seen in yeast two-hybrid assay
n.d.: not done
numberings refer to amino acid positions.

09215543 .072701

5D


GST
Lgs-N
Lgs-C
GST
IVT Arm
GST
Δ-Arm
GST
IVT Lgs

5E

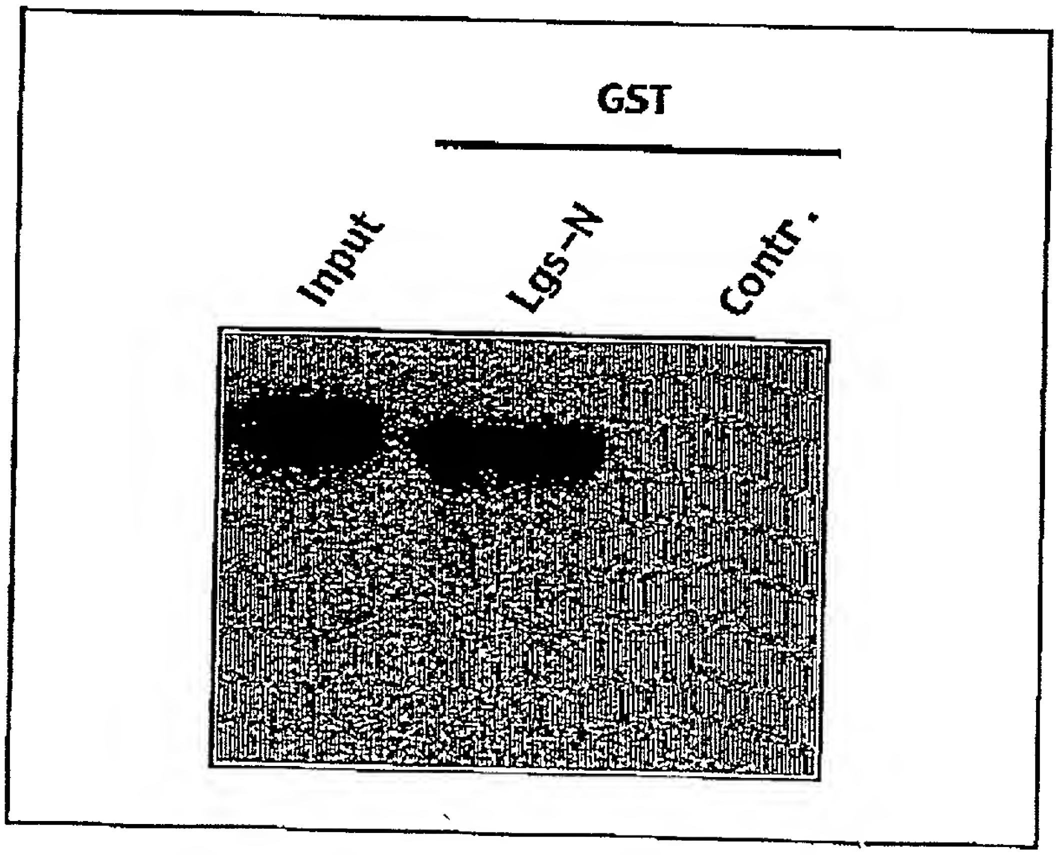

GST
Input
Lgs-N
Contr.

Figure 6

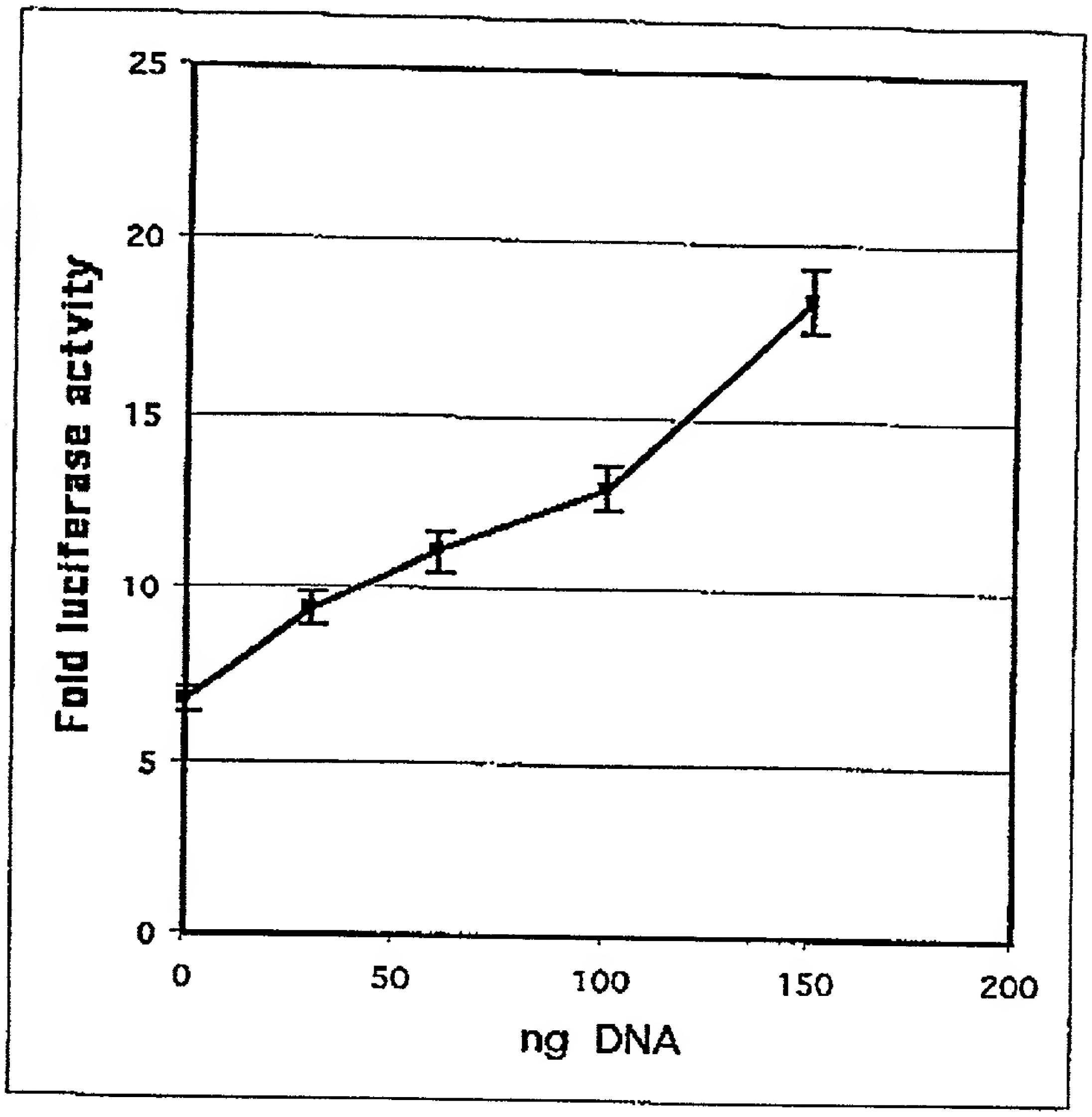
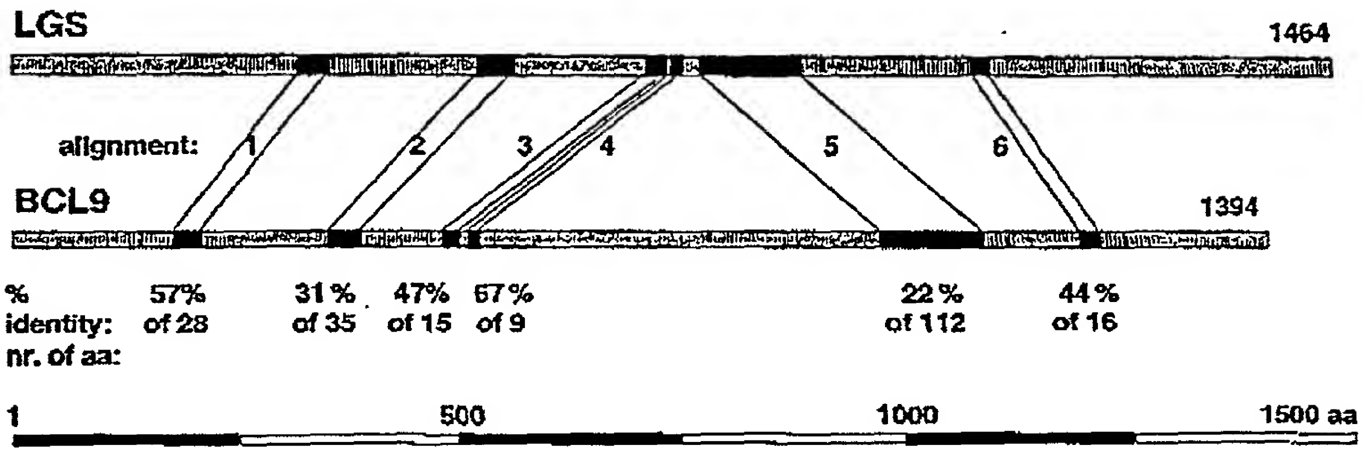


Figure 7

A


LGS
1464
alignment:
1
2
3
4
5
6
BCL9
1394
%
identity:
nr. of aa:
57%
of 28
31 %
of 35
47%
of 15
67 %
of 9
22 %
of 112
44 %
of 16
1
500
1000
1500 aa

09945535 .072701

7B

Sequence homology domain 1: 57.1% identity in 28 aa

```
        320       330       340
LGS     IFVFSTQLANKGAESVLSGQFQTIIAYH
        ..::::..:::.::.:: :: .::...:
BCL9    VYVFSTEMANKAAEAVLKGQVETIVSFH
         180       190       200
```

Sequence homology domain 2: 31.4% identity in 35 aa

```
           520       530       540
LGS     ENLTPQQRQHREEQLAKIKKMNQFLFPENENSVGA
        ..:...: .:::  :  .. ... :::.. . .::
BCL9    DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA
       350       360       370       380
```

Sequence homology domain 3: 46.7% identity in 15 aa

```
          710       720
LGS     QMEWSKIQHQFFEER
        :..: :.:..:.::.
BCL9    QIAWLKLQQEFYEEK
       470       480
```

Sequence homology domain 4: 66.6% identity in 9 aa

```
           760
LGS     LQGPPPPYH
        ..::::::.
BCL9    VRGPPPPYQ
               520
```

Sequence homology domain 5: 22.3% identity in 112 aa

```
        770       780       790       800       810       820
LGS     SASVPIATQSPNPSSPNNLSLPSPRTTAAVMGLPTNSPSMDGTGSLSGSVPQANTSTVQA
        ... :.:.:... . :..:. ..: : ..    :. :. :.    ..: . ....:.  ..
BCL9    GPPPPTASQPASVNIPGSLPSSTPYTMPPEPTLSQNPLSIM-MSRMSKFAMPSSTPLYHD
       970       980       990       1000      1010      1020

        830       840       850       860       870
LGS     GTTTVLSANKNCFQADTPSPSNQNRSRNTGSSSVLTHNLSSNPSTPLSHLSP
        .. :: :.. .  .: .:. .. :    . : ..    .  ..:: .:.. :::
BCL9    AIKTVASSDDDSPPARSPNLPSMNNMPGMGINTQNPRISGPNPVVPMPTLSP
       1030      1040      1050      1060      1070
```

Sequence homology domain 6: 43.8% identity in 16 aa

```
              1080
LGS     NPKMCVAGGPNGPPGF
        .. .: .:::.:: .:

BCL9    DAALCKPGGPGGPDSF
      1190      1200
```

09915575.072501

Figure 8

A

ATGCATTCCAGTAACCCTAAAGTGAGGAGCTCTCCATCAGGAAACACACA
GAGTAGCCCTAAGTCAAAGCAGGAGGTGATGGTCCGTCCCCCTACAGTGA
TGTCCCCATCTGGAAACCCCCAGCTGGATTCCAAATTCTCCAATCAGGGT
AAACAGGGGGGCTCAGCCAGCCAATCCCAGCCATCCCCCTGTGACTCCAA
GAGTGGGGGCCATACCCCTAAAGCACTCCCTGGCCCAGGTGGGAGCATGG
GGCTGAAGAATGGGGCTGGAAATGGTGCCAAGGGCAAGGGGAAAAGGGAG
CGAAGTATTTCCGCCGACTCCTTTGATCAGAGAGATCCTGGGACTCCAAA
CGATGACTCTGACATTAAAGAATGTAATTCTGCTGACCACATAAAGTCCC
AGGATTCCCAGCACACACCACACTCGATGACCCCATCAAATGCTACAGCC
CCCAGGTCTTCTACCCCCTCCCATGGCCAAACTACTGCCACAGAGCCCAC
ACCTGCTCAGAAGACTCCAGCCAAAGTGGTGTACGTGTTTTCTACTGAGA
TGGCCAATAAAGCTGCAGAAGCTGTTTTGAAGGGCCAGGTTGAAACTATC
GTCTCTTTCCACATCCAGAACATTTCTAACAACAAGACAGAGAGAAGCAC
AGCGCCTCTGAACACACAGATATCTGCCCTTCGGAATGATCCGAAACCTC
TCCCACAACAGCCCCCAGCTCCGGCCAACCAGGACCAGAATTCTTCCCAG
AATACCAGACTGCAGCCAACTCCACCCATTCCGGCACCAGCACCCAAGCC
TGCCGCACCCCCACGTCCCCTGGACCGGGAGAGTCCTGGGGTAGAAAACA
AACTGATTCCTTCTGTAGGAAGTCCTGCCAGCTCCACTCCACTGCCCCCA
GATGGTACTGGGCCCAACTCAACTCCCAACAATAGGGCAGTGACCCCTGT
CTCCCAGGGGAGCAATAGCTCTTCAGCAGATCCCAAAGCCCCTCCGCCTC
CACCAGTGTCCAGTGGCGAGCCCCCCACACTGGGAGAGAATCCCGATGGC
CTATCTCAGGAGCAGCTGGAGCACCGGGAGCGCTCCTTACAAACTCTCAG
AGATATCCAGCGCATGCTTTTTCCTGATGAGAAAGAATTCACAGGAGCAC
AAAGTGGGGGACCGCAGCAGAATCCTGGGGTATTAGATGGGCCTCAGAAA
AAACCAGAAGGGCCAATACAGGCCATGATGGCCCAATCCCAAAGCCTAGG
TAAGGGACCTGGGCCCCGGACAGACGTGGGAGCTCCATTTGGCCCTCAAG
GACATAGAGATGTACCCTTTTCTCCAGATGAAATGGTTCCACCTTCTATG
AACTCCCAGTCTGGGACCATAGGACCCGACCACCTTGACCATATGACTCC
CGAGCAGATAGCGTGGCTGAAACTGCAGCAGGAGTTTTATGAAGAGAAGA
GGAGGAAGCAGGAACAAGTGGTTGTCCAGCAGTGTTCCCTCCAGGACATG
ATGGTCCATCAGCACGGGCCTCGGGGAGTGGTCCGAGGACCCCCCCCTCC
ATACCAGATGACCCCTAGTGAAGGCTGGGCACCTGGGGGTACAGAGCCAT
TTTCTGATGGTATCAACATGCCACATTCTCTGCCCCCGAGGGGCATGGCT
CCCCACCCCAACATGCCAGGGAGCCAGATGCGCCTCCCTGGATTTGCAGG
CATGATAAACTCTGAAATGGAAGGGCCGAATGTCCCCAACCCTGCATCTA
GACCAGGTCTTTCTGGAGTCAGTTGGCCAGATGATGTGCCAAAAATCCCA
GATGGTCGAAATTTTCCTCCTGGCCAGGGCATTTTCAGCGGTCCTGGCCG
AGGGGAACGCTTCCCAAACCCCCAAGGATTGTCTGAAGAGATGTTTCAGC
AGCAGCTGGCAGAGAAACAGCTGGGTCTCCCCCCAGGGATGGCCATGGAA
GGCATCAGGCCCAGCATGGAGATGAACAGGATGATTCCAGGCTCCCAGCG
CCACATGGAGCCTGGGAATAACCCCATTTTCCCTCGAATACCAGTTGAGG
GCCCTCTGAGTCCTTCTAGGGGTGACTTTCCAAAAGGAATTCCCCCACAG

09915543.072701

Figure 8A

```
ATGGGCCCTGGTCGGGAACTTGAGTTTGGGATGGTTCCTAGTGGGATGAA
GGGAGATGTCAATCTAAATGTCAACATGGGATCCAACTCTCAGATGATAC
CTCAGAAGATGAGAGAGGCTGGGGCGGGCCCTGAGGAGATGCTGAAATTA
CGCCCAGGTGGCTCAGACATGCTGCCTGCTCAGCAGAAGATGGTGCCACT
GCCATTTGGTGAGCACCCCCAGCAGGAGTATGGCATGGGCCCCAGACCAT
TCCTTCCCATGTCTCAGGGTCCAGGCAGCAACAGTGGCTTGCGGAATCTC
AGAGAACCAATTGGGCCCGACCAGAGGACTAACAGCCGGCTCAGTCATAT
GCCACCACTACCTCTCAACCCTTCCAGTAACCCCACCAGCCTCAACACAG
CTCCTCCAGTTCAGCGCGGCCTGGGGCGGAAGCCCTTGGATATATCTGTG
GCAGGCAGCCAGGTGCATTCCCCAGGCATTAACCCTCTGAAGTCTCCCAC
GATGCACCAAGTCCAGTCACCAATGCTGGGCTCGCCCTCGGGGAACCTCA
AGTCCCCCCAGACTCCATCGCAGCTGGCAGGCATGCTGGCGGGCCCAGCT
GCTGCTGCTTCCATTAAGTCCCCCCCTGTTTTGGGGTCTGCTGCTGCTTC
ACCTGTCCACCTCAAGTCTCCATCACTTCCTGCCCCGTCACCTGGATGGA
CCTCTTCTCCAAAACCTCCCCTTCAGAGTCCTGGGATCCCTCCAAACCAT
AAAGCACCCCTCACCATGGCCTCCCCAGCCATGCTGGGAAATGTAGAGTC
AGGTGGCCCCCCACCTCCTACAGCCAGCCAGCCTGCCTCTGTGAATATCC
CTGGAAGTCTTCCCTCTAGTACACCTTATACCATGCCTCCAGAGCCAACC
CTTTCCCAGAACCCACTCTCTATTATGATGTCTCGAATGTCCAAGTTTGC
AATGCCCAGTTCCACCCCGTTATACCATGATGCTATCAAGACTGTGGCCA
GCTCAGATGACGACTCCCCTCCAGCTCGTTCTCCCAACTTGCCATCAATG
AATAATATGCCAGGAATGGGCATTAATACACAGAATCCTCGAATTTCAGG
TCCAAACCCCGTGGTTCCGATGCCAACCCTCAGCCCAATGGGAATGACCC
AGCCACTTTCTCACTCCAATCAGATGCCCTCTCCAAATGCCGTGGGACCC
AACATACCTCCTCATGGGGTCCCAATGGGGCCTGGCTTGATGTCACACAA
TCCTATCATGGGGCATGGGTCCCAGGAGCCACCGATGGTACCTCAAGGAC
GGATGGGCTTCCCCCAGGGCTTCCCTCCAGTACAGTCTCCCCCACAGCAG
GTTCCATTCCCTCACAATGGCCCCAGTGGGGGGCAGGGCAGCTTCCCAGG
AGGGATGGGTTTCCCAGGAGAAGGCCCCCTTGGCCGCCCCAGCAACCTGC
CCCAAAGTTCAGCAGATGCAGCACTTTGCAAGCCTGGAGGCCCCGGGGGT
CCTGACTCCTTCACTGTCCTGGGGAACAGCATGCCTTCGGTGTTTACAGA
CCCAGATCTGCAGGAGGTCATCCGACCTGGAGCCACCGGAATACCTGAGT
TTGATCTATCCCGCATTATTCCATCTGAGAAGCCCAGCCAGACGCTGCAA
TATTTCCCTCGAGGGGAAGTTCCAGGCCGTAAACAGCCCCAGGGTCCTGG
ACCTGGGTTTTCACACATGCAGGGGATGATGGGCGAACAAGCCCCCAGAA
TGGGACTAGCATTACCTGGCATGGGAGGTCCAGGGCCAGTGGGAACTCCG
GACATCCCTCTTGGTACAGCTCCATCCATGCCAGGCCACAACCCCATGAG
ACCACCAGCCTTTCTCCAACAAGGCATGATGGGACCTCACCATCGGATGA
TGTCACCAGCACAATCTACAATGCCCGGCCAGCCCACCCTGATGAGCAAT
CCAGCTGCTGCCGTGGGCATGATTCCTGGCAAGGATCGGGGGCCTGCCGG
GCTCTACACCCACCCTGGGCCTGTGGGCTCTCCAGGCATGATGATGTCCA
TGCAGGGCATGATGGGACCCCAACAGAACATCATGATCCCCCCACAGATG
AGGCCCCGGGGCATGGCTGCTGACGTGGGCATGGGTGGATTTAGCCAAGG
ACCTGGCAACCCAGGAAACATGATGTTTTAA
```

09615543.072701

Figure 8B

B

MHSSNPKVRSSPSGNTQSSPKSKQEVMVRPPTVMSPSGNPQLDSKFSNQG
KQGGSASQSQPSPCDSKSGGHTPKALPGPGGSMGLKNGAGNGAKGKGKRE
RSISADSFDQRDPGTPNDDSDIKECNSADHIKSQDSQHTPHSMTPSNATA
PRSSTPSHGQTTATEPTPAQKTPAKVVYVFSTEMANKAAEAVLKGQVETI
VSFHIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQ
NTRLQPTPPIPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPP
DGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPTLGENPDG
LSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGAQSGGPQQNPGVLDGPQK
KPEGPIQAMMAQSQSLGKGPGPRTDVGAPFGPQGHRDVPFSPDEMVPPSM
NSQSGTIGPDHLDHMTPEQIAWLKLQQEFYEEKRRKQEQVVVQQCSLQDM
MVHQHGPRGVVRGPPPPYQMTPSEGWAPGGTEPFSDGINMPHSLPPRGMA
PHPNMPGSQMRLPGFAGMINSEMEGPNVPNPASRPGLSGVSWPDDVPKIP
DGRNFPPGQGIFSGPGRGERFPNPQGLSEEMFQQQLAEKQLGLPPGMAME
GIRPSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGPLSPSRGDFPKGIPPQ
MGPGRELEFGMVPSGMKGDVNLNVNMGSNSQMIPQKMREAGAGPEEMLKL
RPGGSDMLPAQQKMVPLPFGEHPQQEYGMGPRPFLPMSQGPGSNSGLRNL
REPIGPDQRTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRGLGRKPLDISV
AGSQVHSPGINPLKSPTMHQVQSPMLGSPSGNLKSPQTPSQLAGMLAGPA
AAASIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSSPKPPLQSPGIPPNH
KAPLTMASPAMLGNVESGGPPPPTASQPASVNIPGSLPSSTPYTMPPEPT
LSQNPLSIMMSRMSKFAMPSSTPLYHDAIKTVASSDDDSPPARSPNLPSM
NNMPGMGINTQNPRISGPNPVVPMPTLSPMGMTQPLSHSNQMPSPNAVGP
NIPPHGVPMGPGLMSHNPIMGHGSQEPPMVPQGRMGFPQGFPPVQSPPQQ
VPFPHNGPSGGQGSFPGGMGFPGEGPLGRPSNLPQSSADAALCKPGGPGG
PDSFTVLGNSMPSVFTDPDLQEVIRPGATGIPEFDLSRIIPSEKPSQTLQ
YFPRGEVPGRKQPQGPGPGFSHMQGMMGEQAPRMGLALPGMGGPGPVGTP
DIPLGTAPSMPGHNPMRPPAFLQQGMMGPHHRMMSPAQSTMPGQPTLMSN
PAAAVGMIPGKDRGPAGLYTHPGPVGSPGMMMSMQGMMGPQQNIMIPPQM
RPRGMAADVGMGGFSQGPGNPGNMMF*

09545743 .072704

Figure 9

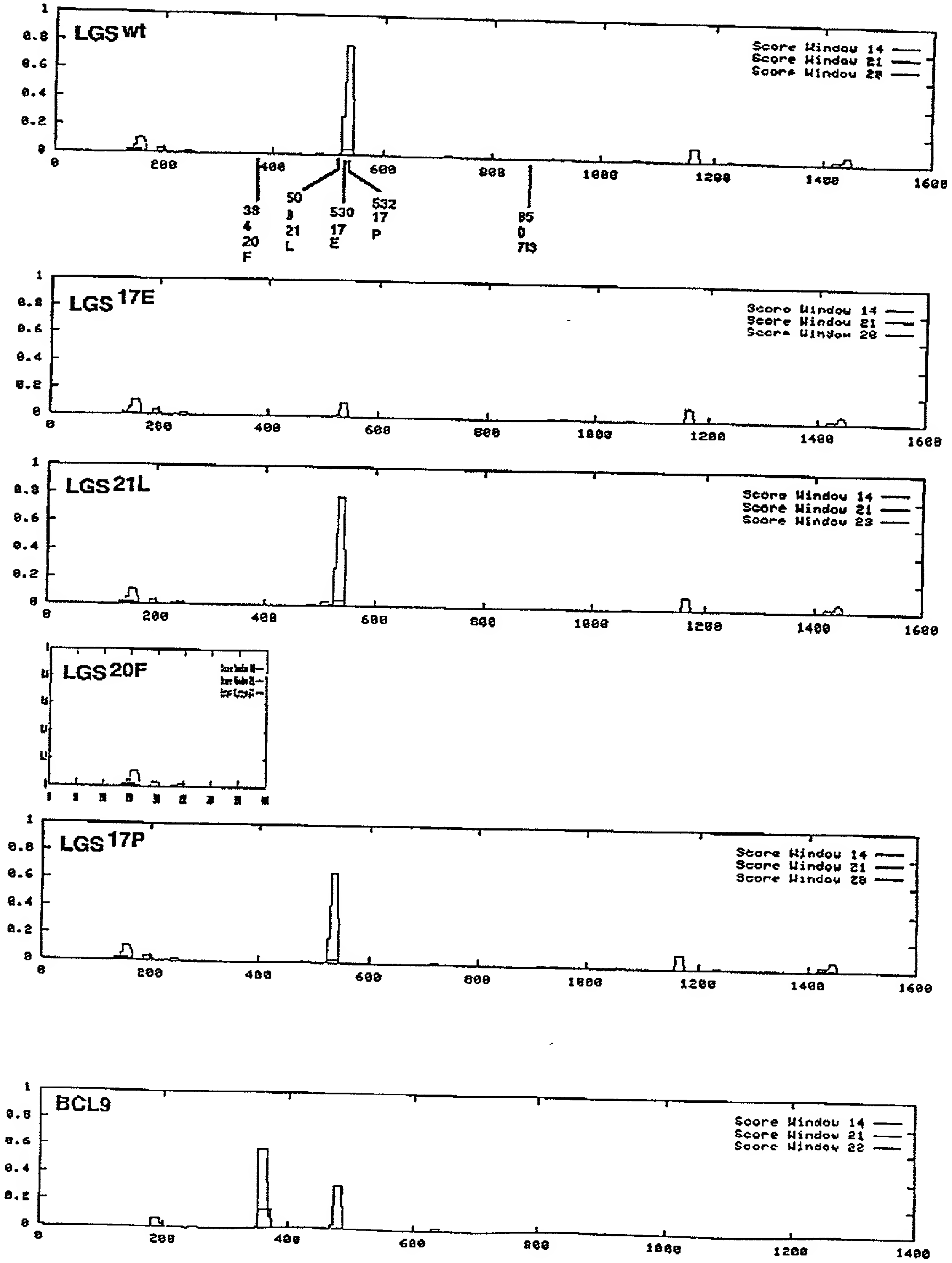

LGS wt
LGS 17E
LGS 21L
LGS 20F
LGS 17P
BCL9
Score Window 14
Score Window 21
Score Window 28
Score Window 22
0
0.2
0.4
0.6
0.8
1
0
200
400
600
800
1000
1200
1400
1600
38
4
20
F
50
8
21
L
530
17
E
532
17
P
85
0
713

Figure 10

A

ATGGCCTGCTTCCCATCCCCTGCTGCCATCTCCTGCACCCTTAGGGCACAGTGGGCATCT
CGGGAGCTGCTCAGCGGACAGACTAGGGTTACCCCCACCCCAGGAGGAGAGAAGCTCCAG
GGAGCCCGCCGCTGTCCCCCGCGGTCATTGCCCCCTGCCCCAGCCAAGCCAATGCACCCA
GAAAATAAATTGACCAATCATGGCAAGACAGGGAATGGCGGGGCCCAATCTCAGCACCAG
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GTGCCCCCTTTCAGCTCGCTCAAGGGCAAGGTGAAGAGGGACCGGAGTGTGTCTGTGGAC
TCTGGAGAGCAGCGAGAGGCTGGACCCCATCCCTGGATTCAGAGGCCAAAGAGGTGGCG
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TGCTCTGGACCGGACAGTGAGGAGGACGACAAGCCCATTGGGGCCACCCACAAAGCTGCT
TTCAAAGAAGACGGCTTTCAGGACAAGGCATCACACTTCTTCTCCAGCACGTACAGTCCT
GAAACCTCCAGGAGGAAGCTGCCCCAAGCCCCGAAGGCTTCCTTCCTGGGGCAGCAGGGC
CGAGTCATTTGGAAACCTCTCTCGGAGGAGCTCCGTGATCAAGGTGCAGATGCGGCAGGT
GGGCCGGCCTCAATCATGTCTCCAATCGCGACGGTGAATGCGAGTGGCTTGTCCAAAGAG
CAGCTGGAGCATCGGGAACGGTCCCTCCAGACGCTGCGAGACATTGAGCGACTGCTGCTC
CGCAGCGGAGAGACTGAGCCCTTCCTCAAGGGGGCCCCCAGGAGGAGCGGCGGGCTGAAG
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CAGGAGGAGTACTACGAAGAGAAACGGCGGAAAGAGGAACAGATTGGGCTGCATGGGAGC
CGTCCTCTGCAGGACATGATGGGCATGGGGGGCATGATGGTGAGGGGGCCCCCGCCTCCT
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GTGCCCATGAATGCCATGCAGAGGCCCGTGAGACCAGGCATGGGCTGGACCGAAGACTTG
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CAGAGCATGGAGATGGAGCGGATGATGCAGGCGCACCGACAGATGGATCCTGCCATGTTT
CCCGGGCAGATGGCTGGTGGTGAGGGCCTGGCGGGCACTCCCATGGGCATGGAGTTTGGT
GGAGGCCGGGGCCTCCTGAGCCCTCCCATGGGGCAGTCTGGGCTGAGGGAGGTGGACCCA
CCCATGGGGCCAGGCAACCTCAACATGAACATGAATGTCAACATGAACATGAACATGAAC
CTGAACGTGCAGATGACCCCGCAGCAGCAGATGCTGATGTCGCAGAAGATGCGGGGCCCT
GGGGACTTGATGGGGCCCCAGGGCCTCAGTCCTGAGGAGATGGCCCGGGTTCGGGCCCAG
AACAGCAGTGGCATGGTGCCCTTGCCTTCTGCCAACCCGCCAGGACCTCTCAAGTCGCCC
CAGGTCCTCGGCTCCTCCCTCAGTGTCCGTTCACCCACTGGCTCGCCCAGCAGGCTCAAG
TCTCCTTCCATGGCGGTGCCTTCTCCAGGCTGGGTTGCCTCACCCAAGACGGCCATGCCC
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CAGGGCTCCGGGCCAGGTGGCCCCGACTCCCTGAATGCCCCCTGTGGCCCAGTGCCCAGC
TCCTCCCAGATGATGCCCTTCCCCCCTCGGCTGCAGCAGCCCCATGGTGCCATGGCCCCC
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TTCCCCAAGAGCGAGAACCAGCCCCCCAAGGCTCAGCCCCCTAATCTGCATCTCATGAAC
CTGCAGAACATGATGGCGGAGCAGACTCCCTCTCGGCCTCCCAACCTCCCAGGCCAGCAG
GGCGATCGGCCGCTGGTGGTGGTGATACCGGGTACCCGGGCTATGGCGCCGGCGCAGCGC
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CAGCGGCAGCTGAAGGAGGCTTTGGAGAGGCTCCTGCCCCAGGTGGAGGCGGCCCGCAAG
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CTGTGCTGCGGCTGTGAGGTGCGGGAACACCTGAGCCATGGAAACCTGACGGTGCTGTAC

09915542.072701

Figure 10

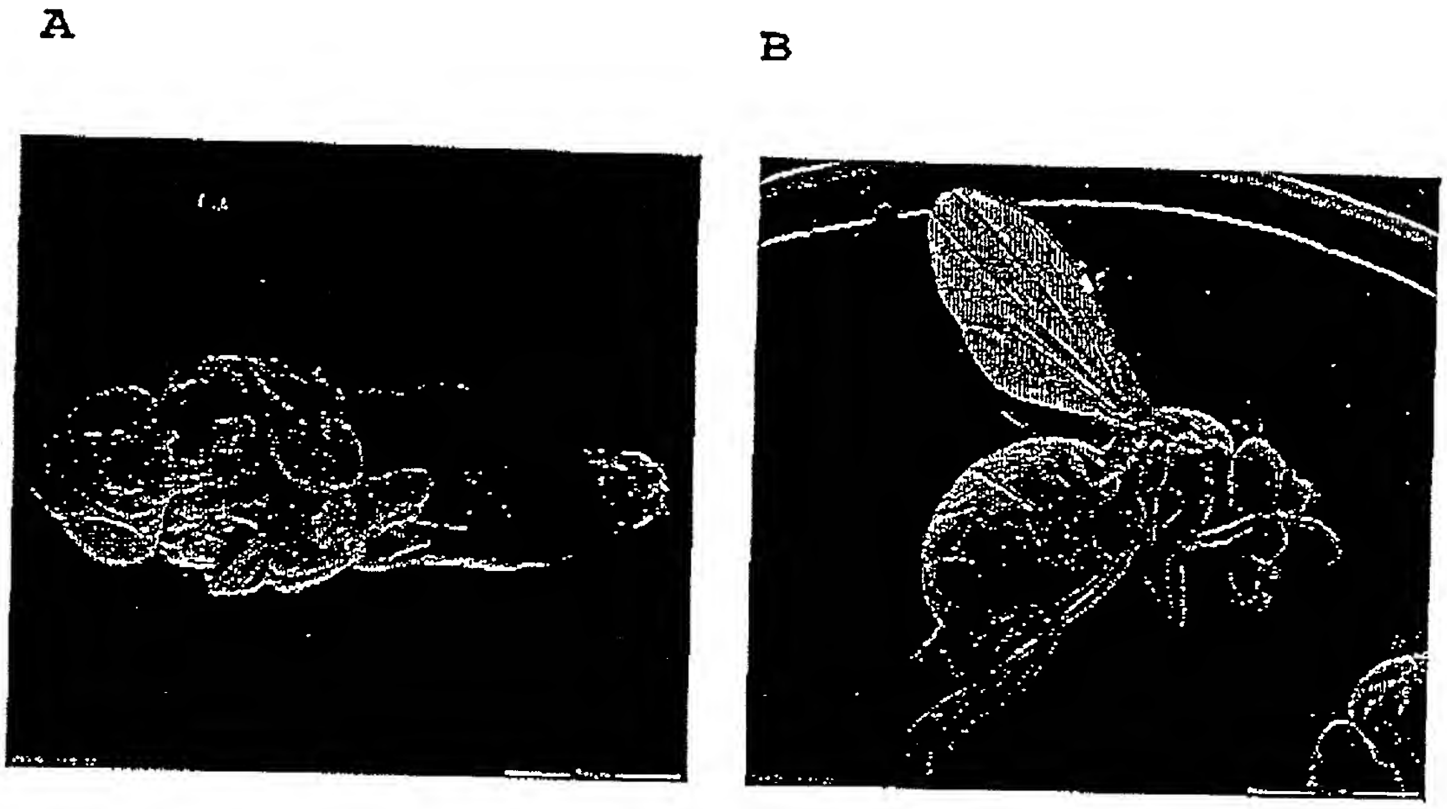
```
GGGGGGCTGCTGGAGCATCTGGCCAGCCCAGAGCACAAGAAAGCAACCAACAAATTCTGG
TGGGAGAACAAAGCTGAGGTCCAGATGAAAGAGAAGTTTCTGGTCACTCCCCAGGATTAT
GCGCGATTCAAGAAATCCATGGTGAAAGGTTTGGATTCCTATGAAGAAAAGGAGGATAAA
GTGATCAAGGAGATGGCAGCTCAGATCCGTGAGGTGGAGCAGAGCCGACAGGAGGTGGTT
CGGTCTGTCTTAGAGACAGGTCCCCCAAGATACGCCCTCACAGTCCGGTCCCCCGCCGTC
CTCTCCCGGCGCACGCTCAAGTCCGGTGCCTTCCCCCCGCAGACCCCCGAGGCGCACCCT
CAAGCTCGGTGCCTCTGCGCCCCCCGCAGGGGCGCCCTCAAGCCTGAGCCCCCCGGGCGC
ACCCTCAAGCTCGGTGTACCCCCCCATACCACCCGCAAGGCGCGCCCTCATGCCGCGAAG
ACTTCGCCCCGCCCAAGGTGCACCCGTCAAGCCCCGAATAAAACCCAGTCACTCCAACTT
GCAGGCAAAGCTAGAAAAACTGCGCTGCATTTGCAAACAAAAGCTCTTGTTGGCGATGAC
GATACTGTTTTGGGTGTGAAACTGTCAATTGCTAACTACGATCTGTGA
```

B

```
RKEDGFQDKASHFFSSTYSPETSRRKLPQAPKASFLGQQGRVIWKPLSEE
LRDQGADAAGGPASIMSPIATVNASGLSKEQLEHRERSLQTLRDIERLLL
RSGETEPFLKGAPRRSGGLKKYEEPLQSMISQTQSLGGPPLEHEVPGHPP
GGDMGQQMNMMIQRLGQDSLTPEQVAWRKLQEEYYEEKRRKEEQIGLHGS
RPLQDMMGMGGMMVRGPPPPYHSKPGDQWPPGMGAQLRGPMDVQDPMQLR
GGPPFPGPRFPGNQIQRVPGFGGMQSMPMEVPMNAMQRPVRPGMGWTEDL
PPMGGPSNFAQNTMPYPGGQGEAERFMTPRVREELLRHQLLEKRSMGMQR
PLGMAGSGMGQSMEMERMMQAHRQMDPAMFPGQMAGGEGLAGTPMGMEFG
GGRGLLSPPMGQSGLREVDPPMGPGNLNMNMNVNMNMNMNLNVQMTPQQQ
MLMSQKMRGPGDLMGPQGLSPEEMARVRAQNSSGMVPLPSANPPGPLKSP
QVLGSSLSVRSPTGSPSRLKSPSMAVPSPGWVASPKTAMPSPGVSQNKQP
PLNMNSSTTLSNMEQDPTPSQNPLSLMMTQMSKYAMPSSTPLYHNAIKTI
ATSDDELLPDRPLLPPPPPPQGSGPGGPDSLNAPCGPVPSSSQMMPFPPR
LQQPHGAMAPTGGGGGGPGLQQHYPSGMALPPEDLPNQPPGPMPPQQHLM
GKAMAGRMGDAYPPGVLPGVASVLNDPELSEVIRPTPTGIPEFDLSRIIP
SEKPSSTLQYFPKSENQPPKAQPPNLHLMNLQNMMAEQTPSRPPNLPGQQ
GDRPLVVVIPGTRAMAPAQRCPLCRQTFFCGRGHVYSRKHQRQLKEALER
LLPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEVREHLSHGNLTVLY
GGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSMVKG
LDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLETGPPRYALTVRSPAV
LSRRTLKSGAFPPQTPEAHPQARCLCAPRRGALKPEPPGRTLKLGVPPHT
TRKARPHAAKTSPRPRCTRQAPNKTQSLQLAGKARKTALHLQTKALVGDD
DTVLGVKLSIANYDL
```

09155473 .070401

Figure 11



09915543 .072701

Figure 12

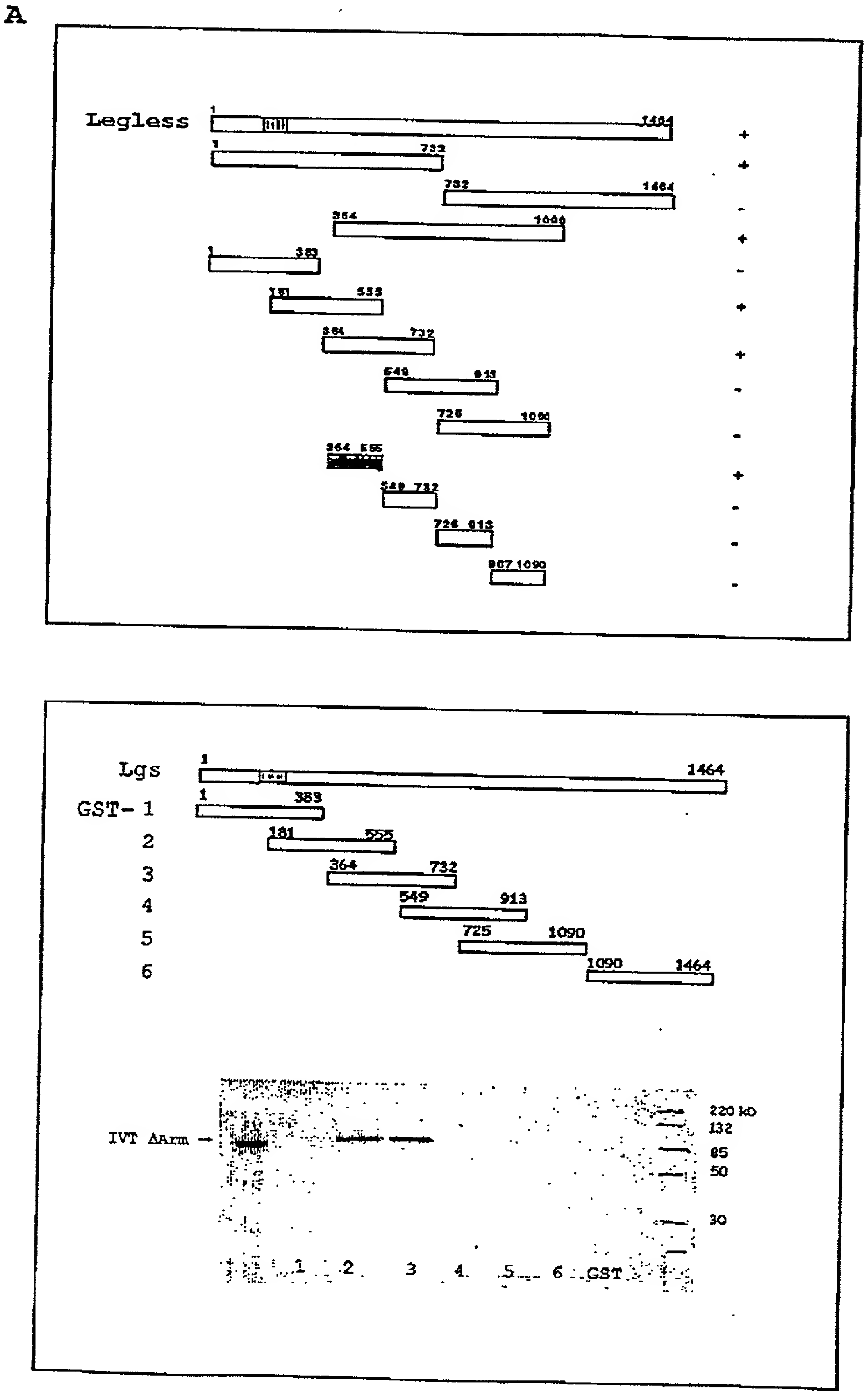

A
Legless
+
+
-
+
-
+
+
-
-
364 555
+
549 732
-
726 913
-
907 1090
-
Lgs
GST- 1
IVT ΔArm →
220 kD
GST

Figure 12B

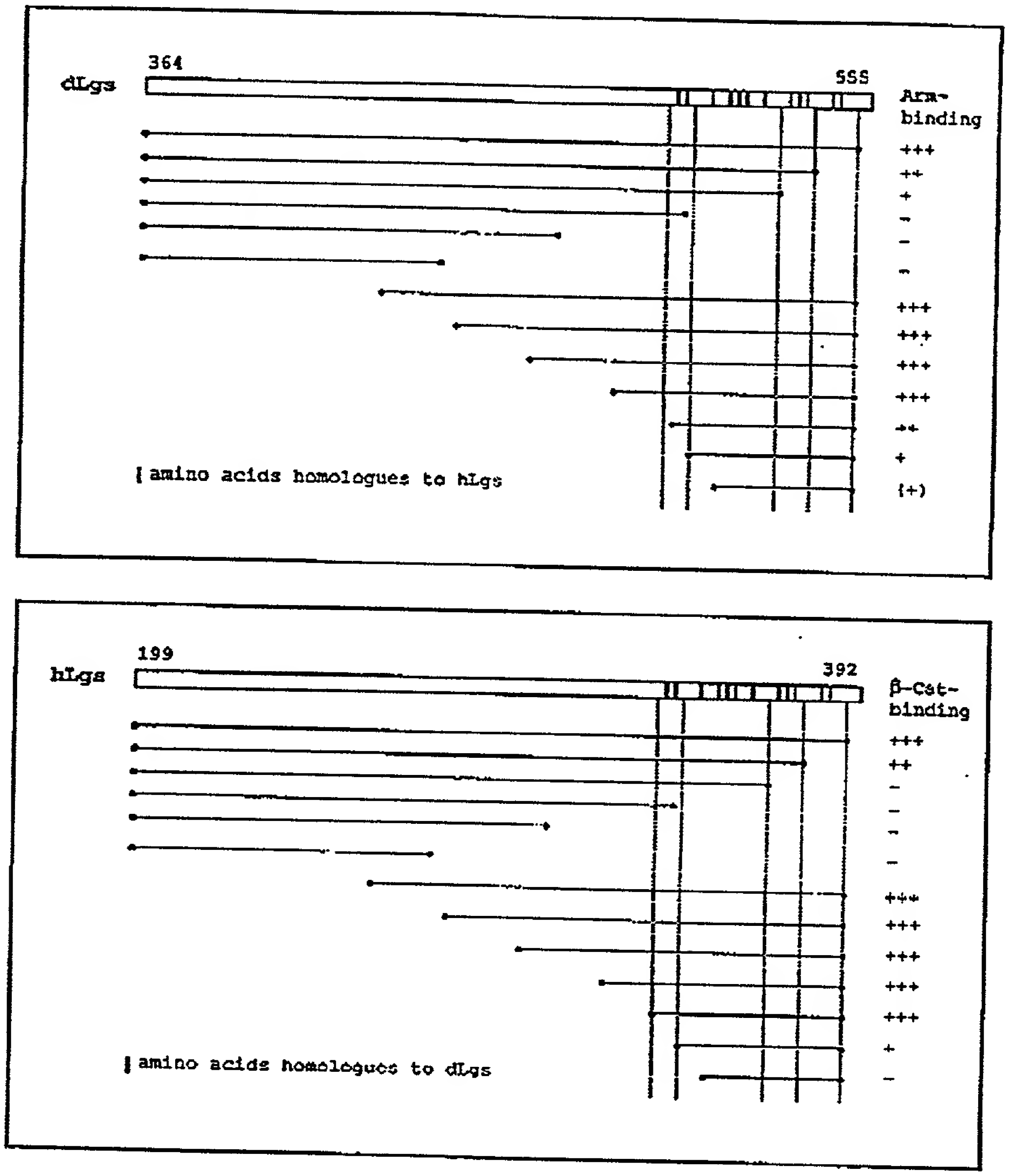

dLgs
364
555
Arm-binding
+++
++
+
-
-
-
+++
+++
+++
+++
++
+
(+)
| amino acids homologues to hLgs
hLgs
199
392
β-Cat-binding
+++
++
-
-
-
-
+++
+++
+++
+++
+++
+
-
| amino acids homologues to dLgs

Figure 12C

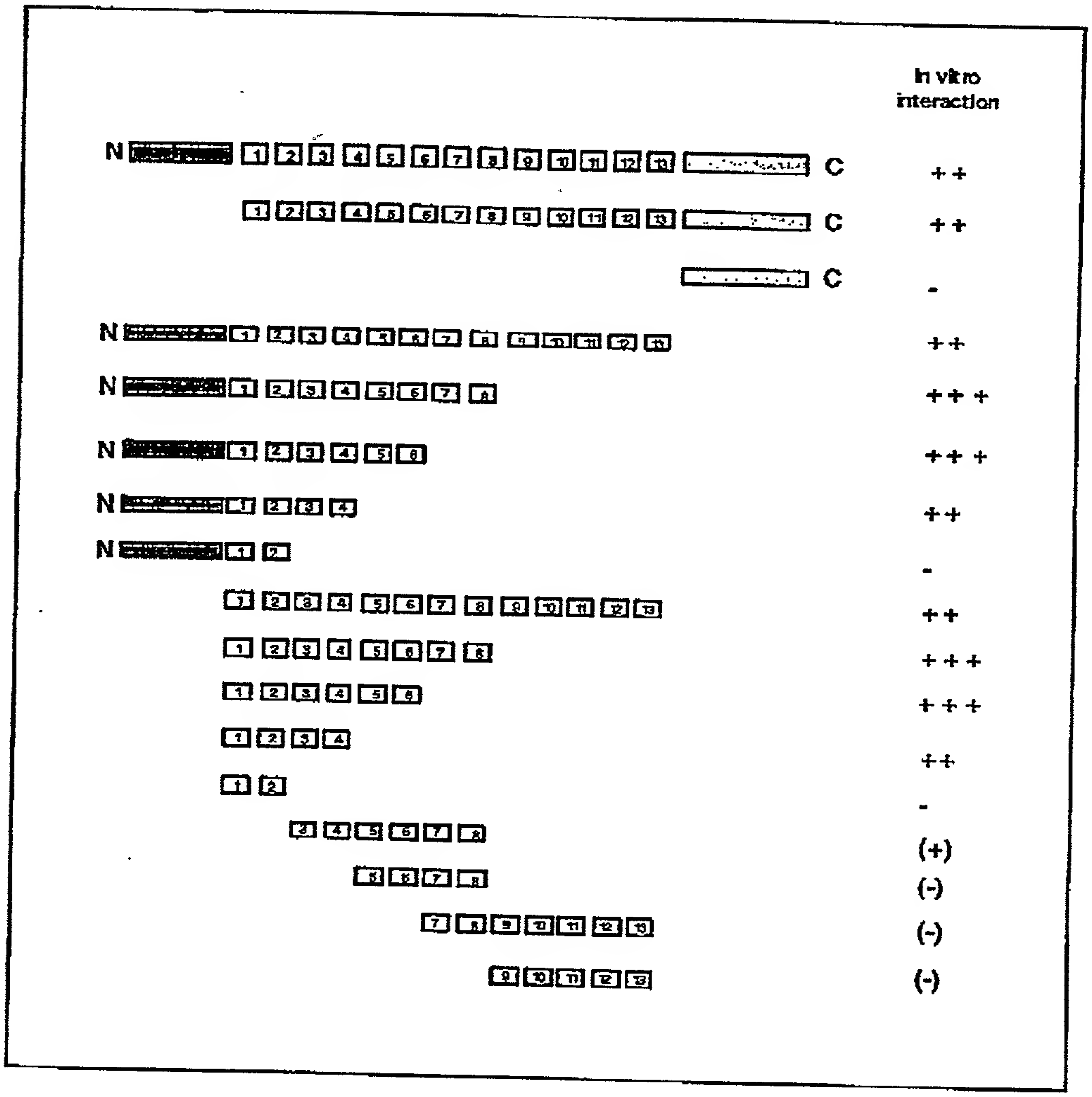

In vitro interaction
N
C
1
2
3
4
5
6
7
8
9
10
11
12
13
++
++
-
++
+++
+++
++
-
++
+++
+++
++
-
(+)
(-)
(-)
(-)

Figure 13

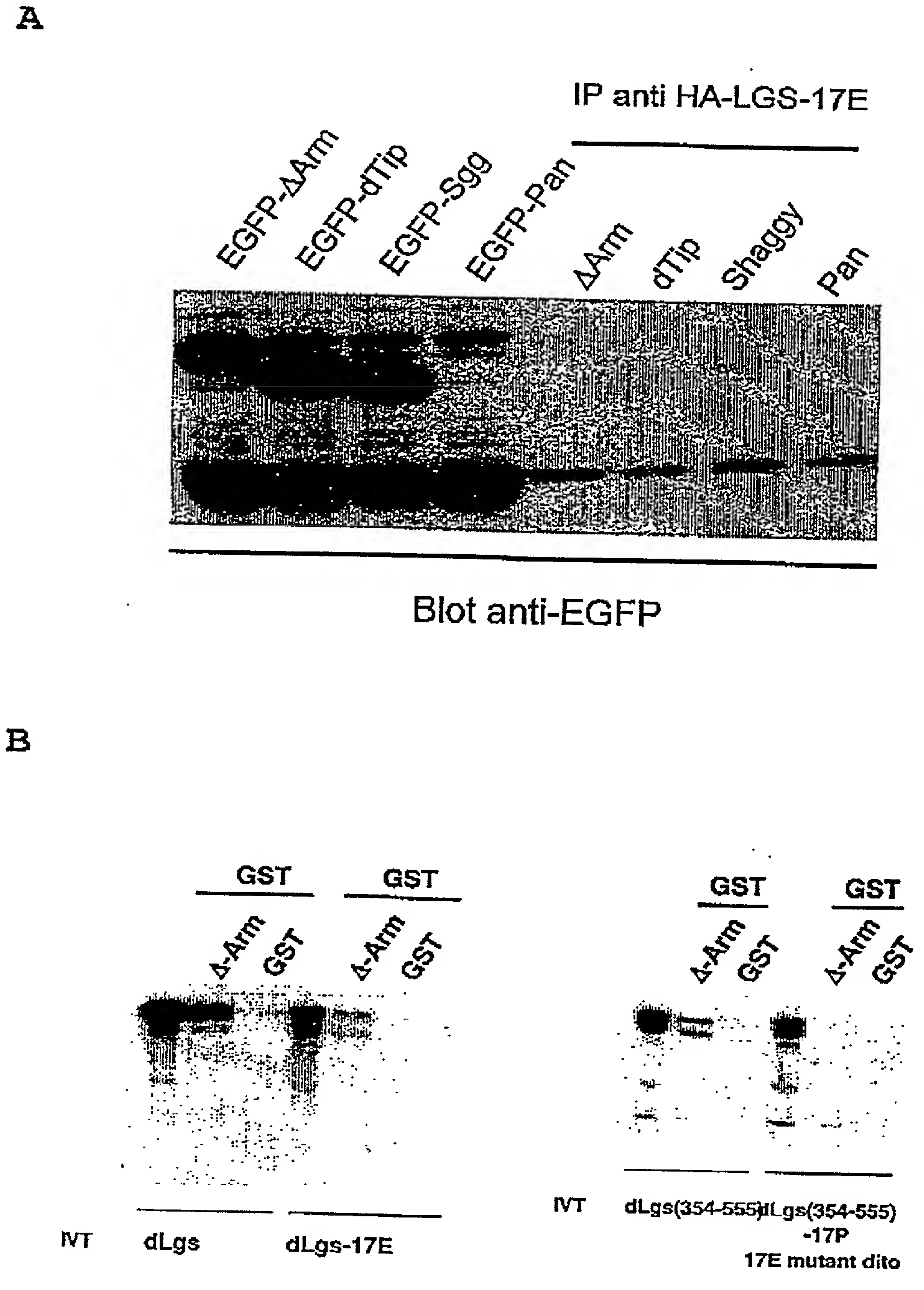

A
IP anti HA-LGS-17E
EGFP-ΔArm
EGFP-dTip
EGFP-Sgg
EGFP-Pan
ΔArm
dTip
Shaggy
Pan
Blot anti-EGFP
B
GST
GST
Δ-Arm
GST
Δ-Arm
GST
IVT
dLgs
dLgs-17E
GST
GST
Δ-Arm
GST
Δ-Arm
GST
IVT
dLgs(354-555)
dLgs(354-555)
-17P
17E mutant dito

Figure 13

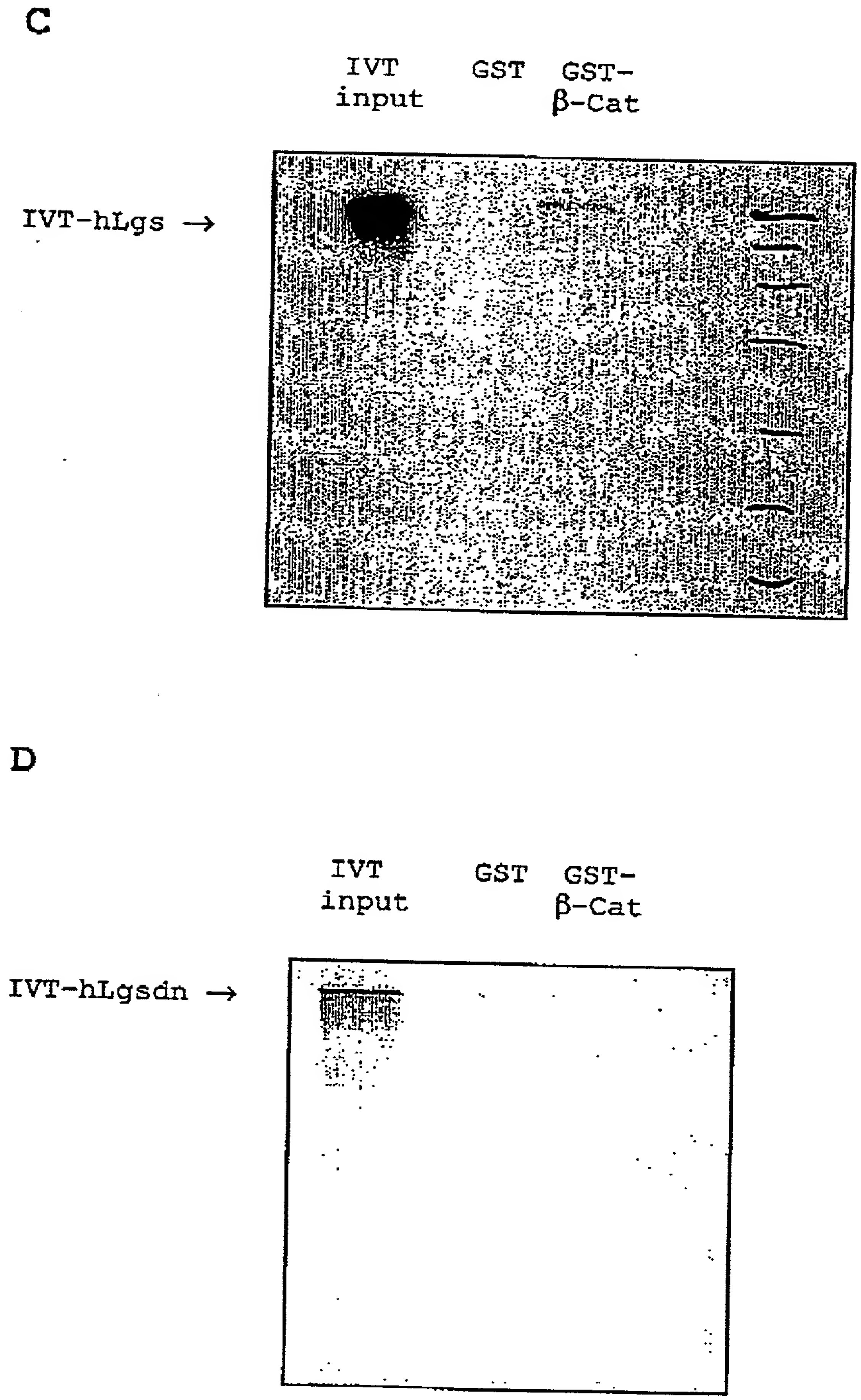
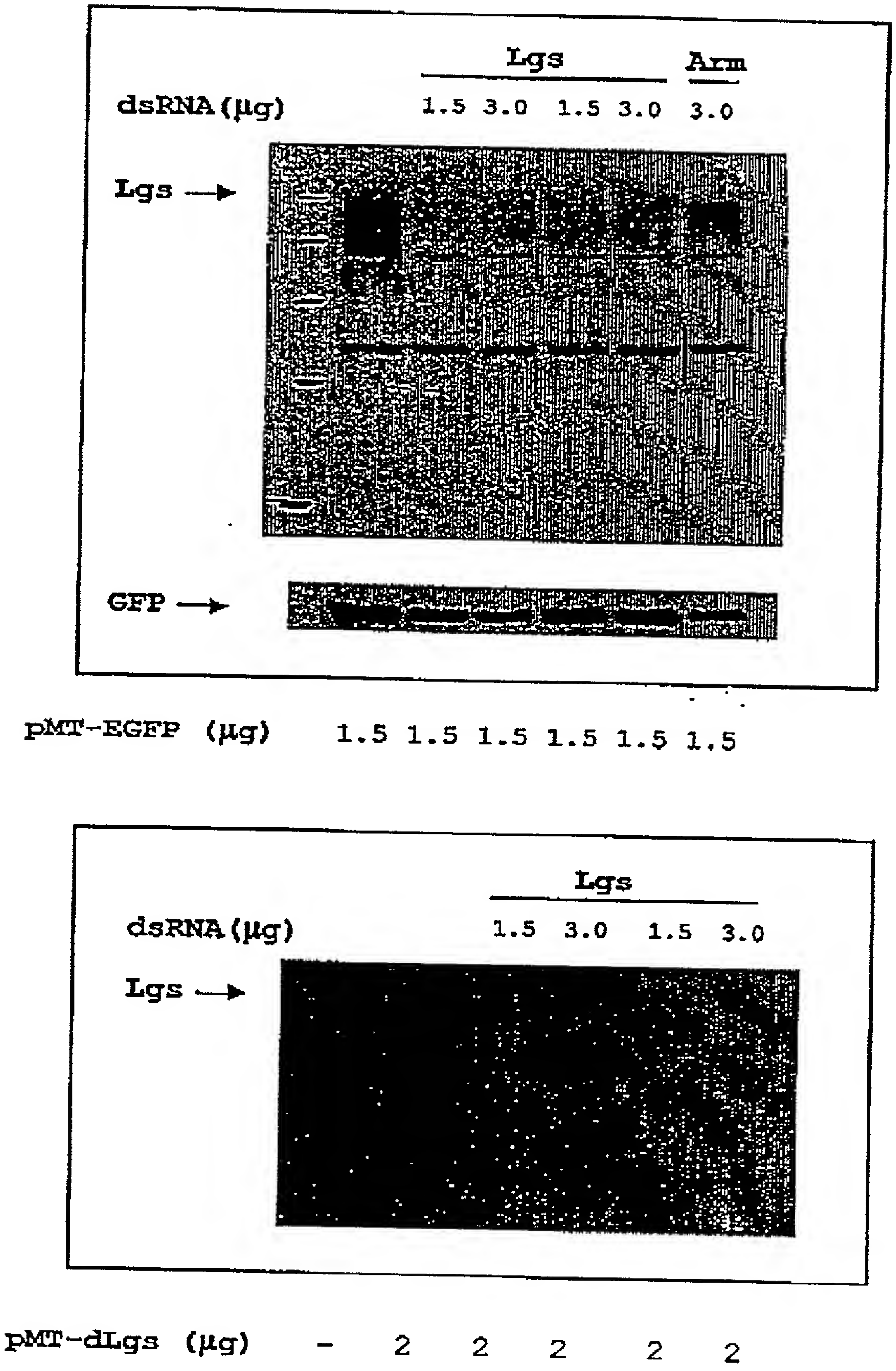

C
IVT input
GST
GST-β-Cat
IVT-hLgs →
D
IVT input
GST
GST-β-Cat
IVT-hLgsdn →

Figure 14


Lgs
Arm
dsRNA (µg) 1.5 3.0 1.5 3.0 3.0
Lgs →
GFP →
pMT-EGFP (µg) 1.5 1.5 1.5 1.5 1.5 1.5
Lgs
dsRNA (µg) 1.5 3.0 1.5 3.0
Lgs →
pMT-dLgs (µg) - 2 2 2 2 2

09555543.062701

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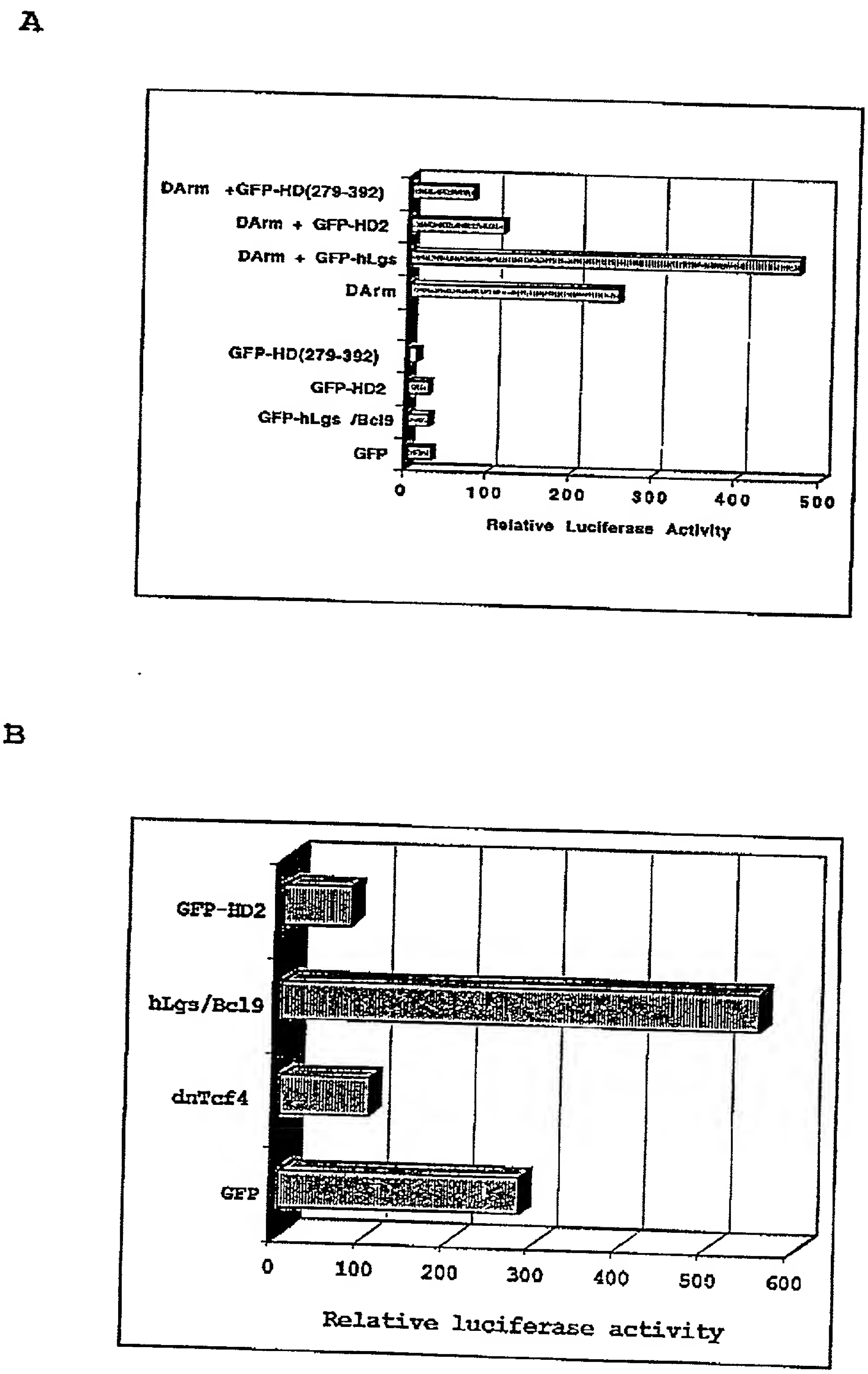
Figure 15



09915543 .072701